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Distribution of Adhesion and Toxin Genes in *Staphylococcus aureus* Strains Recovered From Hospitalized Patients Admitted to the ICU

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Abstract

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) strains are a common cause of emerging nosocomial infections and are a major public health concern.
Objectives: The aim of the present study was to determine the prevalence of MRSA, its antibiotic resistance pattern, and the virulence gene profiles in hospitalized patients admitted to ICUs.
Methods: During a 6-month period, a total of 70 *S. aureus* isolates were collected from 249 patients admitted to the ICU in five hospitals. In vitro antibiotic susceptibility testing of the *S. aureus* isolates was carried out using the Kirby-Bauer disk diffusion method with 16 antibiotic disks. Molecular detection of toxin and adhesion genes was carried out using PCR.
Results: All the 70 *S. aureus* isolates were confirmed to be MRSA strains. The largest number of *S. aureus* isolates was found in the blood (42.9%) and wound (21.4%) samples. The MDR pattern was detected in 71.4% of the isolates, which were obtained from wound and blood samples. Simultaneous resistance to seven, six, five, four and three drugs was common in 35 (50%), 7 (10%), 8 (11.4%), 11 (15.7%), 2 (2.9%) and 5 (7.1%) isolates, respectively. The frequency of the spa, *fnbB*, *fnbA*, *clfB*, *clfA*, *can*, *bbp*, *ebp*, *etb*, *eta*, *pvl*, and *tst* genes was 100%, 75.7%, 74.3%, 78.6%, 71.4%24.3%, 0%, 58.6%, 2.9%, 7.1%, 21.4%, and 51.4%, respectively. In addition, among all the examined genes, the *clfB* (78.6%) and *etb* (2.9%) genes had the highest and lowest prevalence respectively.
Conclusions: In the present study, we found a high prevalence of MRSA at the hospitals studied. The findings emphasized the increased prevalence of MRSA isolates containing different toxin and adhesion genes, probably accompanied by antimicrobial resistance. Infection with such isolates worsens the clinical outcomes as well as the morbidity and mortality rates in hospitalized patients in ICUs.

Keywords: ICU, Methicillin-Resistant *Staphylococcus aureus*, Multidrug-Resistant, *Staphylococcus aureus*

1. Background

As a leading cause of infection in hospitals and within communities, *Staphylococcus aureus* is responsible for a wide range of important infections, ranging from wound infections to life-threatening diseases (1). The transmission of this bacterium easily takes place via direct contact, such as touching contaminated hands (or other body parts) and droplet transmission, and via indirect contact, such as through the breathing of contaminated air in the hospital or other environments (2). The most significant factor that contributes to the successful and extensive distribution of this pathogen is the ability of *S. aureus* strains to express a variety of virulence factors and acquire resistance to new antimicrobial agents (3, 4).

There is a broad range of virulence factors whose expression is related to the pathogenesis of *S. aureus* infections. These factors include extracellular proteins with low molecular weight and toxins such as staphylococcal enterotoxins (SEs), staphylokinase, toxic shock syndrome toxin-1 (TST-1), microbial surface components recognizing adhesive matrix molecules (MSCRAMMs), hemolysin (alpha, beta, gamma and delta types), capsular polysaccharides, panton-valentine leukocidin (PVL), lipase, and exfoliative toxins (*eta* and *etb*). The most common cause of biofilm formation is adhesion proteins. Several types of cell wall-associated adhesion proteins have been reported, namely *fnb*, which encodes fibronectin-binding protein; *cna*, which encodes collagen-binding protein; *clf*, which encodes clumping factor; and *ebp*, elastin-binding protein (5-7). TST-1 can cause toxic shock syndrome and ETs cause peeling skin syndrome. PVL is a putative virulence factor that is hypothesized to increase the ability of the bacterium to